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RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/990,415A

DATE: 04/12/2002 PS
TIME: 14:54:27

Input Set : A:\EP.txt
Output Set: N:\CRF3\04122002\I990415A.raw

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      3 <110> APPLICANT: Pharmacia AB
W-->  4 <120> TITLE OF INVENTION: Protein Cluster I
W-->  5 <130> FILE REFERENCE: 00349
W-->  6 <140> CURRENT APPLICATION NUMBER: US/09/990,415A
      7 <141> CURRENT FILING DATE: 2001-11-21
W-->  8 <160> NUMBER OF SEQ ID: 8
      9 <170> SOFTWARE: PatentIn version 3.0
W--> 10 <210> SEQ ID NO: 1
     11 <211> LENGTH: 1232
     12 <212> TYPE: DNA
     13 <213> ORGANISM: human
     15 <220> FEATURE:
     16 <221> NAME/KEY: CDS
     17 <222> LOCATION: (450)..(1232)
     19 <400> SEQUENCE: 1
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     22 accccagttc tggttctgac gccctagctc attccgcaaa tttagggctt gggtctggct    120
     24 tgttcccctc cggctcgaac cacctcttct ctgagccgag ccagctaccg gggctcctgg    180
     26 aattgccacc cctccctggg caccccttgag gcctccgtgg agggacgtca cggggcagag    240
     28 cgggacgtga gcctgagttt gctgcaggcg tgctctgtgt ggtggctggg ttctgccaat    300
     30 ccccgtgccc accgggtggg cgcggccggg aagctcctgc ccctccctgc tggtcggcgt    360
     32 cacgcgtgac gtcccgcgtg atggctggga gggcccggcg gcgacagcgg aggcagagag    420
     34 gaaggcggtt ctgagagctt cagagagcg atg gaa agc aaa atg ggt gaa ttg      473
     35                               Met Glu Ser Lys Met Gly Glu Leu
     36                               1               5
     38 cct tta gac atc aac atc cag gaa cct cgc tgg gac caa agt act ttc      521
     39 Pro Leu Asp Ile Asn Ile Gln Glu Pro Arg Trp Asp Gln Ser Thr Phe
     40     10                  15                  20
     42 ctg ggc aga gcc cgg cac ttt ttc act gtt act gat cct cga aat ctg      569
     43 Leu Gly Arg Ala Arg His Phe Phe Thr Val Thr Asp Pro Arg Asn Leu
     44 25                  30                  35                  40
     46 ctg ctg tcc ggg gca cag ctg gaa gct tct cgg aac atc gtg cag aac      617
     47 Leu Leu Ser Gly Ala Gln Leu Glu Ala Ser Arg Asn Ile Val Gln Asn
     48                  45                  50                  55
     50 tac agg gcc ggc gtg gtg acc cca ggg atc acc gag gac cag ctg tgg      665
     51 Tyr Arg Ala Gly Val Val Thr Pro Gly Ile Thr Glu Asp Gln Leu Trp
     52             60                  65                  70
     54 agg gcc aag tat gtg tat gac tcc gcc ttc cat ccg gac aca ggg gag      713
     55 Arg Ala Lys Tyr Val Tyr Asp Ser Ala Phe His Pro Asp Thr Gly Glu
     56         75                  80                  85
     58 aag gtg gtc ctg att ggc cgc atg tca gcc cag gtg ccc atg aac atg      761
     59 Lys Val Val Leu Ile Gly Arg Met Ser Ala Gln Val Pro Met Asn Met
     60     90                  95                  100
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```
 62 acc atc act ggc tgc atg ctc aca ttc tac agg aag acc cca acc gtg      809
 63 Thr Ile Thr Gly Cys Met Leu Thr Phe Tyr Arg Lys Thr Pro Thr Val
 64 105                 110                 115                 120
 66 gtg ttc tgg cag tgg gtg aat cag tcc ttc aat gcc att gtt aac tac      857
 67 Val Phe Trp Gln Trp Val Asn Gln Ser Phe Asn Ala Ile Val Asn Tyr
 68                 125                 130                 135
 70 tcc aac cgc agt ggt gac act ccc atc act gtg agg cag ctg ggg aca      905
 71 Ser Asn Arg Ser Gly Asp Thr Pro Ile Thr Val Arg Gln Leu Gly Thr
 72             140                 145                 150
 74 gcc tat gtg agt gcc acc act gga gct gtg gcc acg gcc ctg gga ctc      953
 75 Ala Tyr Val Ser Ala Thr Thr Gly Ala Val Ala Thr Ala Leu Gly Leu
 76         155                 160                 165
 78 aaa tcc ctc acc aag cac ctg ccc ccc ttg gtc ggc aga ttt gtg ccc     1001
 79 Lys Ser Leu Thr Lys His Leu Pro Pro Leu Val Gly Arg Phe Val Pro
 80     170                 175                 180
 82 ttt gca gca gtg gca gct gcc aac tgc atc aac atc ccc ctg atg agg     1049
 83 Phe Ala Ala Val Ala Ala Ala Asn Cys Ile Asn Ile Pro Leu Met Arg
 84 185                 190                 195                 200
 86 cag aga gag ctg cag gtg ggc atc ccg gtg gct gat gag gca ggt cag     1097
 87 Gln Arg Glu Leu Gln Val Gly Ile Pro Val Ala Asp Glu Ala Gly Gln
 88                 205                 210                 215
 90 agg ctt ggc tac tcg gtg act gca gcc aag cag gga atc ttc cag gtg     1145
 91 Arg Leu Gly Tyr Ser Val Thr Ala Ala Lys Gln Gly Ile Phe Gln Val
 92             220                 225                 230
 94 gtg att tca aga atc tgc atg gcg att cct gcc atg gcc atc cca cca     1193
 95 Val Ile Ser Arg Ile Cys Met Ala Ile Pro Ala Met Ala Ile Pro Pro
 96         235                 240                 245
 98 ctg atc atg gac act ctg gag aag aaa gac ttc ctg aag                 1232
 99 Leu Ile Met Asp Thr Leu Glu Lys Lys Asp Phe Leu Lys
100     250                 255                 260
103 <210> SEQ ID NO: 2
104 <211> LENGTH: 261
105 <212> TYPE: PRT
106 <213> ORGANISM: human
W--> 107 <400> SEQUENCE: 2
108 Met Glu Ser Lys Met Gly Glu Leu Pro Leu Asp Ile Asn Ile Gln Glu
109 1               5                  10                  15
111 Pro Arg Trp Asp Gln Ser Thr Phe Leu Gly Arg Ala Arg His Phe Phe
112             20                  25                  30
114 Thr Val Thr Asp Pro Arg Asn Leu Leu Leu Ser Gly Ala Gln Leu Glu
115         35                  40                  45
117 Ala Ser Arg Asn Ile Val Gln Asn Tyr Arg Ala Gly Val Val Thr Pro
118     50                  55                  60
120 Gly Ile Thr Glu Asp Gln Leu Trp Arg Ala Lys Tyr Val Tyr Asp Ser
121 65                  70                  75                  80
123 Ala Phe His Pro Asp Thr Gly Glu Lys Val Val Leu Ile Gly Arg Met
124                 85                  90                  95
126 Ser Ala Gln Val Pro Met Asn Met Thr Ile Thr Gly Cys Met Leu Thr
127             100                 105                 110
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```
129 Phe Tyr Arg Lys Thr Pro Thr Val Val Phe Trp Gln Trp Val Asn Gln
130         115                 120                 125
132 Ser Phe Asn Ala Ile Val Asn Tyr Ser Asn Arg Ser Gly Asp Thr Pro
133     130                 135                 140
135 Ile Thr Val Arg Gln Leu Gly Thr Ala Tyr Val Ser Ala Thr Thr Gly
136 145                 150                 155                 160
138 Ala Val Ala Thr Ala Leu Gly Leu Lys Ser Leu Thr Lys His Leu Pro
139                 165                 170                 175
141 Pro Leu Val Gly Arg Phe Val Pro Phe Ala Ala Val Ala Ala Ala Asn
142             180                 185                 190
144 Cys Ile Asn Ile Pro Leu Met Arg Gln Arg Glu Leu Gln Val Gly Ile
145         195                 200                 205
147 Pro Val Ala Asp Glu Ala Gly Gln Arg Leu Gly Tyr Ser Val Thr Ala
148     210                 215                 220
150 Ala Lys Gln Gly Ile Phe Gln Val Val Ile Ser Arg Ile Cys Met Ala
151 225                 230                 235                 240
153 Ile Pro Ala Met Ala Ile Pro Pro Leu Ile Met Asp Thr Leu Glu Lys
154                 245                 250                 255
156 Lys Asp Phe Leu Lys
157             260
160 <210> SEQ ID NO: 3
161 <211> LENGTH: 1061
162 <212> TYPE: DNA
163 <213> ORGANISM: human
W--> 164 <220> FEATURE:
165 <221> NAME/KEY: CDS
166 <222> LOCATION: (450)..(680)
W--> 167 <400> SEQUENCE: 3
168 cccttaggcg ccagggacag ccgagcgtta cctggtcccg ggcagcggag ttctttaccc     60
170 accccagttc tggttctgac gccctagctc attccgcaaa tttagggctt gggtctggct    120
172 tgttcccctc cggctcgaac cacctcttct ctgagccgag ccagctaccg gggctcctgg    180
174 aattgccacc cctccctggg cacccttgag gcctccgtgg agggacgtca cggggcagag    240
176 cgggacgtga gcctgagttt gctgcaggcg tgctctgtgt ggtggctggg ttctgccaat    300
178 ccccgtgccc accgggtggg cgcggccggg aagctcctgc ccctccctgc tggtcggcgt    360
180 cacgcgtgac gtcccgcgtg atggctggga gggcccggcg gcgacagcgg aggcagagag    420
182 gaaggcggtt ctgagagctt cagagagcg atg gaa agc aaa atg ggt gaa ttg      473
183                                  Met Glu Ser Lys Met Gly Glu Leu
184                                  1               5
186 cct tta gac atc aac atc cag gaa cct cgc tgg gac caa agt act ttc      521
187 Pro Leu Asp Ile Asn Ile Gln Glu Pro Arg Trp Asp Gln Ser Thr Phe
188     10                  15                  20
190 ctg ggc aga gcc cgg cac ttt ttc act gtt act gat cct cga aat ctg      569
191 Leu Gly Arg Ala Arg His Phe Phe Thr Val Thr Asp Pro Arg Asn Leu
192 25                  30                  35                  40
194 ctg ctg tcc ggg gca cag ctg gaa gct tct cgg aac atc gtg cag aac      617
195 Leu Leu Ser Gly Ala Gln Leu Glu Ala Ser Arg Asn Ile Val Gln Asn
196                 45                  50                  55
198 tac agg aag acc cca acc gtg gtg ttc tgg cag tgg gtg aat cag tcc      665
199 Tyr Arg Lys Thr Pro Thr Val Val Phe Trp Gln Trp Val Asn Gln Ser
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```
200             60                  65                  70
202 ttc aat gcc att gtt aactactcca accgcagtgg tgacactccc atcactgtga      720
203 Phe Asn Ala Ile Val
204         75
206 ggcagctggg gacagcctat gtgagtgcca ccactggagc tgtggccacg gccctgggac    780
208 tcaaatccct caccaagcac ctgccccccc tggtcggcag atttgtgccc tttgcagcag    840
210 tggcagctgc caactgcatc aacatccccc tgatgaggca gagagagctg caggtgggca    900
212 tcccggtggc tgatgaggca ggtcagaggc ttggctactc ggtgactgca gccaagcagg    960
214 gaatcttcca ggtggtgatt tcaagaatct gcatggcgat tcctgccatg gccatcccac   1020
216 cactgatcat ggacactctg gagaagaaag acttcctgaa g                       1061
219 <210> SEQ ID NO: 4
220 <211> LENGTH: 77
221 <212> TYPE: PRT
222 <213> ORGANISM: human
W--> 223 <400> SEQUENCE: 4
224 Met Glu Ser Lys Met Gly Glu Leu Pro Leu Asp Ile Asn Ile Gln Glu
225 1               5                  10                  15
227 Pro Arg Trp Asp Gln Ser Thr Phe Leu Gly Arg Ala Arg His Phe Phe
228             20                  25                  30
230 Thr Val Thr Asp Pro Arg Asn Leu Leu Leu Ser Gly Ala Gln Leu Glu
231         35                  40                  45
233 Ala Ser Arg Asn Ile Val Gln Asn Tyr Arg Lys Thr Pro Thr Val Val
234     50                  55                  60
236 Phe Trp Gln Trp Val Asn Gln Ser Phe Asn Ala Ile Val
237 65                  70                  75
240 <210> SEQ ID NO: 5
241 <211> LENGTH: 1567
242 <212> TYPE: DNA
243 <213> ORGANISM: human
W--> 244 <220> FEATURE:
245 <221> NAME/KEY: CDS
246 <222> LOCATION: (47)..(1015)
W--> 247 <400> SEQUENCE: 5
248 gggcatttgt cccgggacca ggtccacagt tttatgtgtg agcaag atg gag gct        55
249                                                    Met Glu Ala
250                                                    1
252 gac ctg tct ggc ttt aac atc gat gcc ccc cgt tgg gac cag cgc acc      103
253 Asp Leu Ser Gly Phe Asn Ile Asp Ala Pro Arg Trp Asp Gln Arg Thr
254     5                  10                  15
256 ttc ctg ggg aga gtg aag cac ttc cta aac atc acg gac ccc cgc act      151
257 Phe Leu Gly Arg Val Lys His Phe Leu Asn Ile Thr Asp Pro Arg Thr
258 20                  25                  30                  35
260 gtc ttt gta tct gag cgg gag ctg gac tgg gcc aag gtg atg gtg gag      199
261 Val Phe Val Ser Glu Arg Glu Leu Asp Trp Ala Lys Val Met Val Glu
262                 40                  45                  50
264 aag agc agg atg ggg gtt gtg ccc cca ggc acc caa gtg gag cag ctg      247
265 Lys Ser Arg Met Gly Val Val Pro Pro Gly Thr Gln Val Glu Gln Leu
266             55                  60                  65
268 ctg tat gcc aag aag ctg tat gac tcg gcc ttc cac ccc gac act ggg      295
```

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Input Set : A:\EP.txt
Output Set: N:\CRF3\04122002\I990415A.raw

```
269 Leu Tyr Ala Lys Lys Leu Tyr Asp Ser Ala Phe His Pro Asp Thr Gly
270         70                  75                  80
272 gag aag atg aat gtc atc ggg cgc atg tct ttc cag ctt cct ggc ggc      343
273 Glu Lys Met Asn Val Ile Gly Arg Met Ser Phe Gln Leu Pro Gly Gly
274     85                  90                  95
276 atg atc atc acg ggc ttc atg ctc cag ttc tac agg acg atg ccg gcg      391
277 Met Ile Ile Thr Gly Phe Met Leu Gln Phe Tyr Arg Thr Met Pro Ala
278 100                 105                 110                 115
280 gtg atc ttc tgg cag tgg gtg aac cag tcc ttc aat gcc tta gtc aac      439
281 Val Ile Phe Trp Gln Trp Val Asn Gln Ser Phe Asn Ala Leu Val Asn
282                 120                 125                 130
284 tac acc aac agg aat gcg gct tcc ccc aca tca gtc agg cag atg gcc      487
285 Tyr Thr Asn Arg Asn Ala Ala Ser Pro Thr Ser Val Arg Gln Met Ala
286             135                 140                 145
288 ctt tcc tac ttc aca gcc aca acc act gct gtg gcc acg gct gtg ggc      535
289 Leu Ser Tyr Phe Thr Ala Thr Thr Thr Ala Val Ala Thr Ala Val Gly
290         150                 155                 160
292 atg aac atg ttg aca aag aaa gcg ccg ccc ttg gtg ggc cgc tgg gtg      583
293 Met Asn Met Leu Thr Lys Lys Ala Pro Pro Leu Val Gly Arg Trp Val
294     165                 170                 175
296 ccc ttt gcc gct gtg gct gcg gct aac tgt gtc aat atc ccc atg atg      631
297 Pro Phe Ala Ala Val Ala Ala Ala Asn Cys Val Asn Ile Pro Met Met
298 180                 185                 190                 195
300 cga cag agg gag ctc ata aag gga atc tgc gtg aag gac agg aat gaa      679
301 Arg Gln Arg Glu Leu Ile Lys Gly Ile Cys Val Lys Asp Arg Asn Glu
302                 200                 205                 210
304 aat gag att ggt cat tcc cgg aga gct gcg gcc ata ggc atc acc caa      727
305 Asn Glu Ile Gly His Ser Arg Arg Ala Ala Ala Ile Gly Ile Thr Gln
306             215                 220                 225
308 gta gtt att tct cgg atc acc atg tca gct cct ggg atg atc ttg ctg      775
309 Val Val Ile Ser Arg Ile Thr Met Ser Ala Pro Gly Met Ile Leu Leu
310         230                 235                 240
312 cca gtc atc atg gaa agg ctt gag aaa ttg cac ttc atg cag aaa gtc      823
313 Pro Val Ile Met Glu Arg Leu Glu Lys Leu His Phe Met Gln Lys Val
314     245                 250                 255
316 aag gtc ctg cac gcc cca ttg cag gtc atg ctg agc ggg tgc ttc ctc      871
317 Lys Val Leu His Ala Pro Leu Gln Val Met Leu Ser Gly Cys Phe Leu
318 260                 265                 270                 275
320 atc ttc atg gtg cca gtg gcg tgt ggg ctt ttc cca cag aaa tgt gaa      919
321 Ile Phe Met Val Pro Val Ala Cys Gly Leu Phe Pro Gln Lys Cys Glu
322                 280                 285                 290
324 ttg cca gtt tcc tat ctg gaa ccg aag ctc caa gac act atc aag gcc      967
325 Leu Pro Val Ser Tyr Leu Glu Pro Lys Leu Gln Asp Thr Ile Lys Ala
326             295                 300                 305
328 aag tat gga gaa ctt gag cct tat gtc tac ttc aat aag ggt ctc taa     1015
329 Lys Tyr Gly Glu Leu Glu Pro Tyr Val Tyr Phe Asn Lys Gly Leu
330         310                 315                 320
332 atgccccact tcagcaagga ccagtctatt cccatattca ccagctcctc cttagctacg   1075
334 tgcacacttg tgtcctcctt ccccttgcc aacaaggcct gaaggccagg gtagattggg   1135
```

Use of n and / or Xaa has been detected in the Sequence Listing. Review the Sequence Listing to ensure a corresponding explanation is present in the <220> to <223> fields of each sequence using n or Xaa.

VERIFICATION SUMMARY DATE: 04/12/2002
PATENT APPLICATION: **US/09/990,415A** TIME: 14:54:28

Input Set : **A:\EP.txt**
Output Set: **N:\CRF3\04122002\I990415A.raw**

L:4 M:283 W: Missing Blank Line separator, <120> field identifier
L:5 M:283 W: Missing Blank Line separator, <130> field identifier
L:6 M:283 W: Missing Blank Line separator, <140> field identifier
L:8 M:283 W: Missing Blank Line separator, <160> field identifier
L:10 M:283 W: Missing Blank Line separator, <210> field identifier
L:107 M:283 W: Missing Blank Line separator, <400> field identifier
L:164 M:283 W: Missing Blank Line separator, <220> field identifier
L:167 M:283 W: Missing Blank Line separator, <400> field identifier
L:223 M:283 W: Missing Blank Line separator, <400> field identifier
L:244 M:283 W: Missing Blank Line separator, <220> field identifier
L:247 M:283 W: Missing Blank Line separator, <400> field identifier
L:357 M:283 W: Missing Blank Line separator, <400> field identifier
L:425 M:283 W: Missing Blank Line separator, <220> field identifier
L:428 M:283 W: Missing Blank Line separator, <220> field identifier
L:432 M:283 W: Missing Blank Line separator, <400> field identifier
L:433 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:564 M:283 W: Missing Blank Line separator, <220> field identifier
L:568 M:283 W: Missing Blank Line separator, <400> field identifier